3. (Amended) A WT1 antisense regulatory region negative regulatory element (NRE) comprising at least a portion of the nucleotide sequence shown in SEQ ID NO: 9 or at least a portion of a variant, due to base substitutions, deletions, and/or additions, of the sequence shown in SEQ ID NO: 9.

4. (Amended) A WT1 antisense regulatory region NRE according to claim 3 wherein the NRE comprises the sequence shown in bold in SEQ ID NO: 9, or variants of such a sequence due to base substitutions, deletions and/or additions.

16. (Amended) A method according to claim 15 wherein the PCR assay system uses at least one of the following primers to amplify a region of nucleotide sequence:

Tf: 5'-GGGTGGAGAAGAAGGATATATTTAT-3'. (SEQ ID NO: 1)

Tr: 5'-TAAATATCAAATTAATTTCTCATCC-3'. (SEQ ID NO: 2)

TfN: 5'-GATATATTTATTTATTAGTTTTGGT-3' (SEQ ID NO: 3; nested primer).

Trn: 5'-AAACCCCTATAATTTACCCTCTTC-3' (SEQ ID NO: 4; nested primer).

30. (Amended) A method according to claim 29 wherein the RT-PCR uses the following primer pair

Primer 1: WT18 CTTAGCACTTTCTTCTTGGC (SEQ ID NO: 5)

Primer 2: WITKBF2 TTGCTCAGTGATTGACCAGG. (SEQ ID NO: 6)

IN THE SPECIFICATION

Please replace the paragraph on page 6, lines 6-14 with the following paragraph.

The methylation state may be determined using a PCR-based assay system. Such a PCR-based assay system may involve the use of sodium-metabisulphite. This has the effect of converting all